

# SEQUENCE LISTING

<110> DAI, KEN-SHOW

<120> HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

<130> U014798-3

<140> 10/653,681

<141> 2003-09-02

<160> 6

<170> PatentIn version 3.2

<210> 1

<211> 1090

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

<220>

<221> CDS

<222> (70)..(333)

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro	
1 5 10	
att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa	159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu	
15 20 25 30	
gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc	207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala	
35 40 45	
tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag	255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys	
50 55 60	
atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag	303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys	
65 70 75	
ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaacc tggactgaaa	353
Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser	
80 85	

tataaaccag tgactaacca ggttgagtgt cacccatacc tcacgcagga gaaactgatc	413
cagtactgcc actccaaggg catcaccggt acggcctaca gccccctggg ctctccggat	473
agaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt	533
gctgcaaagc acaaaaaaac cgcagcccag gttctgatcc gtttccatat ccagaggaat	593
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gactttaaat tgagtgatga ggagatggca accataactca gcttcaacag aaactggagg	713
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<212> PRT

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<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Gly	Leu	Gly	Thr	Trp	Lys	Ser	Pro	Leu	Gly	Lys	Val	Lys	Glu	Ala	Val
			20					25					30		

Lys	Val	Ala	Ile	Asp	Ala	Gly	Tyr	Arg	His	Ile	Asp	Cys	Ala	Tyr	Val
		35						40				45			

Tyr	Gln	Asn	Glu	His	Glu	Val	Gly	Glu	Ala	Ile	Gln	Glu	Lys	Ile	Gln
	50					55					60				

Glu	Lys	Ala	Val	Lys	Arg	Glu	Asp	Leu	Phe	Ile	Val	Ser	Lys	Leu	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65

70

75

80

Pro Thr Ser Arg Ser Arg Ser Ser  
85

&lt;210&gt; 3

&lt;211&gt; 1279

&lt;212&gt; DNA

&lt;213&gt; ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;223&gt; VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (70) .. (804)

&lt;400&gt; 3

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gcaccaacc atg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc      111
      Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
        1             5             10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa      159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15             20             25             30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc      207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
        35             40             45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag      255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
        50             55             60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag      303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
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ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag      351
Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu
        80             85             90

aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att      399
Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile
        95             100             105             110

cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat      447
His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp
        115             120             125

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gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg	543
Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly	
145 150 155	
gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct	591
Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro	
160 165 170	
gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac	639
Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr	
175 180 185 190	
ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc	687
Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr	
195 200 205	
gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag	735
Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys	
210 215 220	
cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct	783
Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala	
225 230 235	
gca aag cac tcc cca agt ctg tgacaccagc acgcattgtt gagaacattc	834
Ala Lys His Ser Pro Ser Leu	
240 245	
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 <212> PRT  
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<220>

<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val  
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35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln  
50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp  
65 70 75 80

Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr  
85 90 95

Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp  
100 105 110

Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys  
115 120 125

Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala  
130 135 140

Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser  
145 150 155 160

Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu  
165 170 175

Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr  
180 185 190

Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr

195

200

205

Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu  
 210 215 220

Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys  
 225 230 235 240

His Ser Pro Ser Leu  
 245

&lt;210&gt; 5

&lt;211&gt; 1337

&lt;212&gt; DNA

&lt;213&gt; HOMO SAPIEN

&lt;220&gt;

&lt;223&gt; HUMAN ARL GENE

&lt;400&gt; 5

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gcaggatatt	ggcacattga	ctgtgcctat	gtctatcaga	atgaacatga	agtgggggaa	240
gccatccaag	agaagatcca	agagaaggct	gtgaagcggg	aggacctgtt	catcgctcagc	300
aagttgtggc	ccactttctt	tgagagaccc	cttgtgagga	aagcctttga	gaagaccctc	360
aaggacctga	agctgagcta	tctggacgtc	tatcttattc	actggccaca	gggattcaag	420
tctggggatg	accttttccc	caaagatgat	aaaggtaatg	ccatcggtgg	aaaagcaacg	480
ttcttgatg	cctgggaggc	catggaggag	ctgggtgatg	aggggctggt	gaaagccctt	540
ggggctctcca	atttcagcca	cttcagatc	gagaagctct	tgaacaaacc	tggactgaaa	600
tataaaccag	tgactaacca	ggttgagtgt	caccataacc	tcacgcagga	gaaactgatc	660
cagtactgcc	actccaaggg	catcaccggt	acggcctaca	gccccctggg	ctctccggat	720
agaccttggg	ccaagccaga	agacccttcc	ctgctggagg	atcccaagat	taaggagatt	780
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gactttaaat	tgagtgatga	ggagatggca	accatactca	gcttcaacag	aaactggagg	960
gcctgtaacg	tgttgcaatc	ctctcatttg	gaagactatc	ccttcgatgc	agaatattga	1020
ggttgaatct	cctggtgaga	ttatacagga	gattctcttt	cttcgctgaa	gtgtgactac	1080
ctccactcat	gtccattttt	agccaagctt	atttaagatc	acagtgaact	tagtcctgtt	1140
atagacgaga	atcgaggtgc	tgttttagac	atttatttct	gtatgttcaa	ctaggatcag	1200
aatatcacag	aaaagcatgg	cttgaataag	gaaatgacaa	ttttttccac	ttatctgatc	1260
agaacaaatg	tttattaagc	atcagaaact	ctgccaacac	tgaggatgta	aagatcaata	1320
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&lt;210&gt; 6

<211> 316

<212> PRT

<213> HOMO SAPIEN

<220>

<223> AMINO ACID SEQUENCE ENCODED BY HUMAN ARL GENE

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Gly	Leu	Gly	Thr	Trp	Lys	Ser	Pro	Leu	Gly	Lys	Val	Lys	Glu	Ala	Val	
			20					25						30		
Lys	Val	Ala	Ile	Asp	Ala	Gly	Tyr	Arg	His	Ile	Asp	Cys	Ala	Tyr	Val	
		35					40					45				
Tyr	Gln	Asn	Glu	His	Glu	Val	Gly	Glu	Ala	Ile	Gln	Glu	Lys	Ile	Gln	
	50					55					60					
Glu	Lys	Ala	Val	Lys	Arg	Glu	Asp	Leu	Phe	Ile	Val	Ser	Lys	Leu	Trp	
65					70					75					80	
Pro	Thr	Phe	Phe	Glu	Arg	Pro	Leu	Val	Arg	Lys	Ala	Phe	Glu	Lys	Thr	
				85					90					95		
Leu	Lys	Asp	Leu	Lys	Leu	Ser	Tyr	Leu	Asp	Val	Tyr	Leu	Ile	His	Trp	
			100					105						110		
Pro	Gln	Gly	Phe	Lys	Ser	Gly	Asp	Asp	Leu	Phe	Pro	Lys	Asp	Asp	Lys	
		115					120						125			
Gly	Asn	Ala	Ile	Gly	Gly	Lys	Ala	Thr	Phe	Leu	Asp	Ala	Trp	Glu	Ala	
	130					135						140				
Met	Glu	Glu	Leu	Val	Asp	Glu	Gly	Leu	Val	Lys	Ala	Leu	Gly	Val	Ser	
145					150					155					160	
Asn	Phe	Ser	His	Phe	Gln	Ile	Glu	Lys	Leu	Leu	Asn	Lys	Pro	Gly	Leu	
				165					170						175	
Lys	Tyr	Lys	Pro	Val	Thr	Asn	Gln	Val	Glu	Cys	His	Pro	Tyr	Leu	Thr	
			180					185						190		
Gln	Glu	Lys	Leu	Ile	Gln	Tyr	Cys	His	Ser	Lys	Gly	Ile	Thr	Val	Thr	
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Ala	Tyr	Ser	Pro	Leu	Gly	Ser	Pro	Asp	Arg	Pro	Trp	Ala	Lys	Pro	Glu	
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Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala Ala Lys  
225 230 235 240

His Lys Lys Thr Ala Ala Gln Val Leu Ile Arg Phe His Ile Gln Arg  
245 250 255

Asn Val Ile Val Ile Pro Lys Ser Val Thr Pro Ala Arg Ile Val Glu  
260 265 270

Asn Ile Gln Val Phe Asp Phe Lys Leu Ser Asp Glu Glu Met Ala Thr  
275 280 285

Ile Leu Ser Phe Asn Arg Asn Trp Arg Ala Cys Asn Val Leu Gln Ser  
290 295 300

Ser His Leu Glu Asp Tyr Pro Phe Asp Ala Glu Tyr  
305 310 315